

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
- (ii) TITLE OF INVENTION: Novel CREBa Isoform
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE: Januray 12, 1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Williams Jr., Joseph A.
 - (B) REGISTRATION NUMBER: 38,659
 - (C) REFERENCE/DOCKET NUMBER: 27866/33469
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 312-474-6300
 - (B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 304..1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG	ACTTTCTTGG	GATGAGCGCT	GCCTTTTTTG	CTTCCTTTTG	GATGCACAGC	60
CCGATTTAAC	CCCTGCACCT	TCCGCCCGAT	CCCAGCAGGC	TTGTCCTCCC	CGGGGAGTCA	120
CAGATTTCCG	AGGACAAGGG	TCGCGTAGCC	TTCGGCAGGG	CTCTCCCGAG	TTCCTGCTCC	180
AGTGCATAAG	TTCCACGCGC	GCACACGCCA	AGTACACGGG	GAGAAGCGTC	TCACCGGCCC	240
GCGGCGGCTC	TGCGCGGTCC	CCTCCTGCCT	CAGCATCCTC	GGGCCTGCGC	GGCGCCCACC	300
GCC ATG GAG GTG CTG GAG AGC GGG GAG CAG AGC GTC CTG CAG TGG GAC	348					
Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp						
1 5 10 15						
CGC AAG CTG AGC GAG CTG TCA GAG CCC GGA GAG ACT GAG GCC CTC ATG	396					
Arg Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met						
20 25 30						
TAC CAC ACG CAC TTC TCG GAG CTC CTA GAC GAG TTT TCC CAG AAC GTC	444					
Tyr His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val						
35 40 45						
CTG GGT CAG CTC CTG AGT GAC CCT TTC CTC TCA GAG AAG AGC GAG TCA	492					
Leu Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser						
50 55 60						
ATG GAG GTG GAG CCA TCT CCA ACA TCA CCA GCG CCT CTC ATC CAG GCT	540					
Met Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala						
65 70 75						
GAA CAC AGC TAC TCT CTG AGC GAG GAG CCC CGG ACT CAG TCA CCA TTT	588					
Glu His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe						
80 85 90 95						
ACC CAT GCG GCT ACC AGC GAC AGC TTC AAT GAC GAG GAG GTG GAG AGT	636					
Thr His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser						
100 105 110						
GAA AAA TGG TAC CTG TCT ACA GAG TTT CCT TCA GCT ACC ATC AAG AAA	684					
Glu Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys						
115 120 125						
GAG CCA ATC ACA GAG GAG CAG CCC CCG GGA CTT GTC CCT TCT GTC ACT	732					
Glu Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr						
130 135 140						
CTG ACC ATC ACA GCC ATT TCC ACT CCT TTT GAA AAA GAA GAG TCC CCT	780					
Leu Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro						
145 150 155						
CTG GAT ATG AAT GCT GGG GGG GAC TCC TCA TGC CAG ACG CTT ATT CCT	828					

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Leu	Asp	Met	Asn	Ala	Gly	Gly	Asp	Ser	Ser	Cys	Gln	Thr	Leu	Ile	Pro	
160					165					170					175	
AAG	ATT	AAG	CTG	GAG	CCC	CAC	GAA	GTG	GAT	CAG	TTC	TTA	AAC	TTC	TCC	876
Lys	Ile	Lys	Leu	Glu	Pro	His	Glu	Val	Asp	Gln	Phe	Leu	Asn	Phe	Ser	
				180					185					190		
CCG	AAA	GAA	GCC	TCC	GTG	GAT	CAA	CTG	CAC	TTA	CCA	CCA	ACA	CCA	CCC	924
Pro	Lys	Glu	Ala	Ser	Val	Asp	Gln	Leu	His	Leu	Pro	Pro	Thr	Pro	Pro	
			195					200					205			
AGT	AGT	CAC	AGC	AGT	GAC	TCT	GAG	GGC	AGC	TTG	AGC	CCC	AAC	CCA	CGC	972
Ser	Ser	His	Ser	Ser	Asp	Ser	Glu	Gly	Ser	Leu	Ser	Pro	Asn	Pro	Arg	
		210					215					220				
CTG	CAT	CCC	TTC	AGC	CTG	TCT	CAG	GCC	CAC	AGC	CCT	GTC	AGA	GCC	ATG	1020
Leu	His	Pro	Phe	Ser	Leu	Ser	Gln	Ala	His	Ser	Pro	Val	Arg	Ala	Met	
	225					230					235					
CCC	CGG	GGC	CCC	TCT	GCC	TTG	TCC	ACA	TCT	CCT	CTC	CTC	ACA	GCT	CCA	1068
Pro	Arg	Gly	Pro	Ser	Ala	Leu	Ser	Thr	Ser	Pro	Leu	Leu	Thr	Ala	Pro	
240					245					250					255	
CAT	AAG	CTG	CAG	GGA	TCG	GGC	CCC	CTG	GTC	CTG	ACA	GAA	GAG	GAG	AAG	1116
His	Lys	Leu	Gln	Gly	Ser	Gly	Pro	Leu	Val	Leu	Thr	Glu	Glu	Glu	Lys	
			260						265					270		
AGG	ACC	CTG	GTT	GCC	GAG	GGC	TAT	CCC	ATT	CCC	ACC	AAG	CTG	CCT	CTG	1164
Arg	Thr	Leu	Val	Ala	Glu	Gly	Tyr	Pro	Ile	Pro	Thr	Lys	Leu	Pro	Leu	
		275						280					285			
ACA	AAA	TCT	GAG	GAG	AAG	GCC	CTG	AAG	AAA	ATC	CGG	AGA	AAG	ATC	AAG	1212
Thr	Lys	Ser	Glu	Glu	Lys	Ala	Leu	Lys	Lys	Ile	Arg	Arg	Lys	Ile	Lys	
		290					295					300				
AAT	AAG	ATT	TCT	GCC	CAA	GAA	AGC	AGG	AGA	AAG	AAG	AAA	GAA	TAC	ATG	1260
Asn	Lys	Ile	Ser	Ala	Gln	Glu	Ser	Arg	Arg	Lys	Lys	Lys	Glu	Tyr	Met	
	305					310					315					
GAC	AGC	CTG	GAG	AAA	AAA	GTG	GAG	TCT	TGT	TCA	ACT	GAG	AAC	TTG	GAG	1308
Asp	Ser	Leu	Glu	Lys	Lys	Val	Glu	Ser	Cys	Ser	Thr	Glu	Asn	Leu	Glu	
320					325					330					335	
CTT	CGG	AAG	AAG	GTG	GAG	GTG	CTG	GAG	AAC	ACC	AAT	AGG	ACT	CTC	CTT	1356
Leu	Arg	Lys	Lys	Val	Glu	Val	Leu	Glu	Asn	Thr	Asn	Arg	Thr	Leu	Leu	
				340					345					350		
CAG	CAA	CTT	CAG	AAG	CTT	CAG	ACT	TTG	GTG	ATG	GGG	AAG	GTC	TCT	CGA	1404
Gln	Gln	Leu	Gln	Lys	Leu	Gln	Thr	Leu	Val	Met	Gly	Lys	Val	Ser	Arg	
		355						360					365			
ACC	TGC	AAG	TTA	GCT	GGC	ACA	CAG	ACT	GGC	ACC	TGC	CTC	ATG	GTC	GTT	1452
Thr	Cys	Lys	Leu	Ala	Gly	Thr	Gln	Thr	Gly	Thr	Cys	Leu	Met	Val	Val	
		370					375						380			

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GTG CTT TGC TTT GCT GTT GCA TTT GGA AGC TTC TTT CAA GGC TAT GGG Val Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly 385 390 395	1500
CCT TAT CCT TCT GCC ACC AAG ATG GCT CTG CCC AGC CAG CAT CCT CTG Pro Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu 400 405 410 415	1548
TCA GAG CCA TAC ACA GCC TCC GTG GTG AGA TCC AGG AAC CTG CTA ATC Ser Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile 420 425 430	1596
TAT GAG GAA CAC GCT CCC CTG GAA GAG TCG TCG AGC CCA GCC TCA ACC Tyr Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr 435 440 445	1644
GGG GAG CTG GGG GGC TGG GAC AGA GGC TCC TCT CTG CTC AGG GCA TCG Gly Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser 450 455 460	1692
TCG GGG CTT GAG GCC CTG CCA GAG GTG GAT CTT CCC CAT TTC CTT ATC Ser Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile 465 470 475	1740
TCC AAT GAG ACG AGC TTG GAG AAG TCA GTA CTG TTG GAG CTT CAG CAG Ser Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln 480 485 490 495	1788
CAC CTG GTC AGC AGC AAA CTG GAA GGG AAC GAA ACA CTC AAG GTT GTA His Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val 500 505 510	1836
GAG CTG GAG AGG AGA GTG AAC GCC ACC TTC TGAGGAGAGC TCCACCCTCC Glu Leu Glu Arg Arg Val Asn Ala Thr Phe 515 520	1886
TCTTCTCCTA ACTCCATCTG ATCGTCCTTT CAGTTTCCCC TTCACCACTG GATCTCGAGG	1946
AGGAGATGGC TAGTGTTACG GCTCGAGACA GGAGGCCAGC CCAGGGGGTT CTGCTTATGT	2006
GTCCCCGTGG CTCTCCACAA AAGGGAGCTA GCACCTCTCC ATCCCTTTCT CTTACTGCCA	2066
TTGGAAATTA TTTTAGGGCT GAGATAGGGG TGGAACGAGC AGGCTTGTTT CCACCAATAG	2126
TGCCAAGAAG ACACTGCCTG ATTCTTCCCC GGGAGGAGTG ACTCCTCTGA AGAAGACATG	2186
ACTCATGTTC AGTTGAGACC CCAGACTCTA GCCACACACA TGCCACAGAC ATGCCAGGGA	2246
GTGGCAAAGC ACTGACTCCT GAGCTCCCTT CCTCACTAGG ACTCCAGTGT GACCCTGCAC	2306
TGAGAGGACC AAAGCGTCAT TGCAGTCTTC TCTCCACCCT GTACCCCGGA GTCCTGATTG	2366
GATGTCTGCA GAGGCAGATG GGGCTCCAC CATATTTTCA GGCCGCAAGT GCAATTCCTG	2426

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AAGGCATCAG GCTCTTCTCT CCCAGGCTCT CCTGCCCCACT GTGTTGTTTG TAGGACACCC 2486
 CCACACCCAC TCATACACAG CCTGCATCTC CACAGGACAA TAGCTCTGTC TCCCTGGCCT 2546
 CCCCTCCCCA TTTGTAAATA GTATTTATTA GCTTGCTCAA GCTCCCAGCT GGCCATAGTG 2606
 AAAAGATTTT CCCTTTCAAC CAGCAAAGTC TTCTGTTGGC CTTTGAACA GGAGAGTCCC 2666
 CGGAATCTAG GACCCTAGTC TTTGTACTTG ATGCCTTGTT TCCCCCTTT TCTTCTTTAA 2726
 AATTGGGGAC CTATAACATC ATCGCTGTTG CGGAATCCAC TTAGGCATGT GTCCCCTGAT 2786
 GGATGAATAC ATGGGAATGG TGGATACTGT CTTCTGACTC AGGCTCTAGG CTCCATGGCT 2846
 TCCTCTCTCT GGTCCTGCCA CACAGAAGGA AAGCCCTGTC CAGGATAATG AGCGTTGCTG 2906
 ACACCCTTGC TAGCTTGTC TGCCTACCTG CTTACCCAC TCCCTCACCT TCCTCCTTCC 2966
 CTTCTGCCCT CCATCCACCT GCCTTAACTA ATTGGGGCTG GAGTTGGTCA TTTTTTGTAC 3026
 ACCCACAGTG GTACCTTTTA CAGTCAGGTT TGGATACTTT GCAGCTCATC CAAAGAGACA 3086
 TAACTAAACC CTAAACTCTT TTTTGTGTGT TGTGTTGTT GTTTTTTTTT TTTATGATTA 3146
 AAAAGTAAAA ATTGTAGTTT AAAAAAAAAA AAAAAAACT CGAG 3190

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg
 1 5 10 15
 Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr
 20 25 30
 His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu
 35 40 45
 Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met
 50 55 60
 Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu
 65 70 75 80
 His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr

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85					90					95					
His	Ala	Ala	Thr	Ser	Asp	Ser	Phe	Asn	Asp	Glu	Glu	Val	Glu	Ser	Glu
			100					105					110		
Lys	Trp	Tyr	Leu	Ser	Thr	Glu	Phe	Pro	Ser	Ala	Thr	Ile	Lys	Lys	Glu
		115					120					125			
Pro	Ile	Thr	Glu	Glu	Gln	Pro	Pro	Gly	Leu	Val	Pro	Ser	Val	Thr	Leu
	130					135					140				
Thr	Ile	Thr	Ala	Ile	Ser	Thr	Pro	Phe	Glu	Lys	Glu	Glu	Ser	Pro	Leu
	145					150					155				160
Asp	Met	Asn	Ala	Gly	Gly	Asp	Ser	Ser	Cys	Gln	Thr	Leu	Ile	Pro	Lys
				165					170					175	
Ile	Lys	Leu	Glu	Pro	His	Glu	Val	Asp	Gln	Phe	Leu	Asn	Phe	Ser	Pro
		180						185					190		
Lys	Glu	Ala	Ser	Val	Asp	Gln	Leu	His	Leu	Pro	Pro	Thr	Pro	Pro	Ser
		195					200					205			
Ser	His	Ser	Ser	Asp	Ser	Glu	Gly	Ser	Leu	Ser	Pro	Asn	Pro	Arg	Leu
	210					215					220				
His	Pro	Phe	Ser	Leu	Ser	Gln	Ala	His	Ser	Pro	Val	Arg	Ala	Met	Pro
	225					230					235				240
Arg	Gly	Pro	Ser	Ala	Leu	Ser	Thr	Ser	Pro	Leu	Leu	Thr	Ala	Pro	His
				245					250					255	
Lys	Leu	Gln	Gly	Ser	Gly	Pro	Leu	Val	Leu	Thr	Glu	Glu	Glu	Lys	Arg
		260					265					270			
Thr	Leu	Val	Ala	Glu	Gly	Tyr	Pro	Ile	Pro	Thr	Lys	Leu	Pro	Leu	Thr
	275						280					285			
Lys	Ser	Glu	Glu	Lys	Ala	Leu	Lys	Lys	Ile	Arg	Arg	Lys	Ile	Lys	Asn
	290					295					300				
Lys	Ile	Ser	Ala	Gln	Glu	Ser	Arg	Arg	Lys	Lys	Lys	Glu	Tyr	Met	Asp
	305					310					315				320
Ser	Leu	Glu	Lys	Lys	Val	Glu	Ser	Cys	Ser	Thr	Glu	Asn	Leu	Glu	Leu
				325					330					335	
Arg	Lys	Lys	Val	Glu	Val	Leu	Glu	Asn	Thr	Asn	Arg	Thr	Leu	Leu	Gln
			340					345					350		
Gln	Leu	Gln	Lys	Leu	Gln	Thr	Leu	Val	Met	Gly	Lys	Val	Ser	Arg	Thr
	355						360					365			
Cys	Lys	Leu	Ala	Gly	Thr	Gln	Thr	Gly	Thr	Cys	Leu	Met	Val	Val	Val

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370 375 380

Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro
385 390 395 400

Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser
 405 410 415

Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr
 420 425 430

Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly
 435 440 445

Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser
 450 455 460

Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser
465 470 475 480

Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His
 485 490 495

Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu
 500 505 510

Leu Glu Arg Arg Val Asn Ala Thr Phe
 515 520

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGATCCT AATGGAGCTG AGAGTCGGG

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGATCCG CTCATCGGTG CACGACAGA

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ACAGCTCCAC ATAAGCTGC

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAATTCGCT CAAGGAGAGT CCTATTGG

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGTCAGTT CAGCGGATCC TGTCGNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
NNNNNNNNNG AGGCGAATTC AGTGCAACTG CAGC 154

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTCAGTT CAGCGGATCC TGTCG 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGCAGTTG CACTGAATTC GCCTC 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATCGGGCC GCCGAGATCT CATATGGAGC TGAGAGTC

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